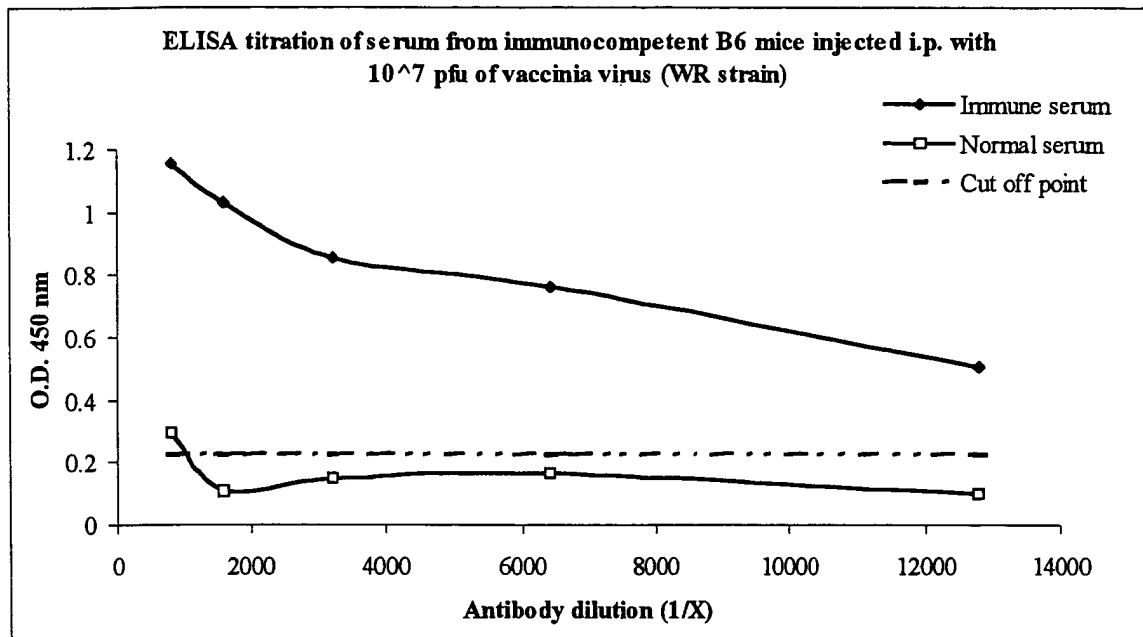
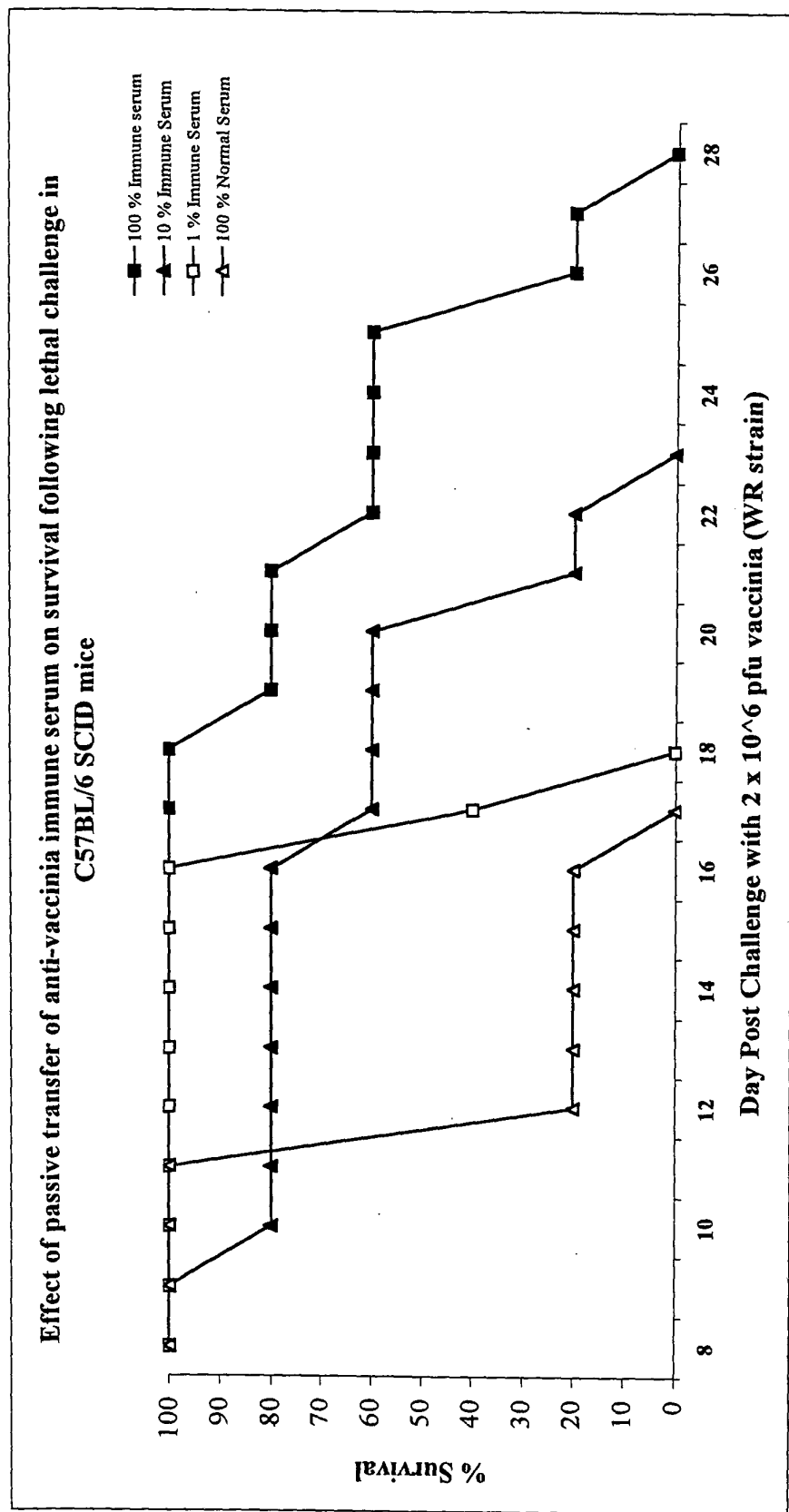


Fig 1



Wells were coated with 100  $\mu$ l of vaccinia stock ( $2.5 \times 10^8$  pfu per ml) diluted 1:100 in sodium bicarbonate buffer for 1 hour at 37°C. After washing three times with 0.05 % (v:v) PBS/Tween 20, the plate was blocked with 200  $\mu$ l of 10% bovine serum albumin in PBS/Tween 20 for 1 hr. The plate was again washed and 100  $\mu$ l of a two-fold dilution series of murine serum was added to triplicate wells for 1 hour at 37°C. After subsequent washing, 100  $\mu$ l of goat-anti-mouse HRP conjugated antibody diluted 1:1000 was added to each well for 1 hour at 37°C. The plate was washed again as before and 100  $\mu$ l of Sure Blue (TM) TMB peroxidase substrate (KPL, Gaithersburg, MD) was added. After allowing 5 min for color development, 100  $\mu$ l of Sure Blue (TM) stop solution was added to each well and the plate was read at 450 nm. The cut off point was defined as the mean of the data points shown for normal mouse serum + 3 standard deviations.

Fig. 2



# L1R-M1Ralign

							Section 1
	(1)	1	10	20	30	40	54
L1R-P07612	(1)	MGAAASIQTTVNTLSERISSKLEQEANASAQTKCDIEIGNFYIRQNHGCNLTVK					
L1R-AAA48076	(1)	MGAAASIQTTVNTLSERISSKLEQEANASAQTKCDIEIGNFYIRQNHGCNLTVK					
M1R-AAA60821	(1)	MGAAASIQTTVNTLSERISSKLEQEANASAQTKCDIEIGNFYIRQNHGCNLTVK					
M1R-P33040	(1)	MGAAASIQTTVNTLSERISSKLEQEANASAQTKCDIEIGNFYIRQNHGCNLTVK					
Consensus	(1)	MGAAASIQTTVNTLSERISSKLEQEANASAQTKCDIEIGNFYIRQNHGCNLTVK					
							Section 2
	(55)	55	60	70	80	90	108
L1R-P07612	(55)	NMCSADADAQLDAVLSAATETYSGLTPEQKAYVPAMFTAALNIQTSVNTVVRDF					
L1R-AAA48076	(55)	NMCSADADAQLDAVLSAATETYSGLTPEQKAYVPAMFTAALNIQTSVNTVVRDF					
M1R-AAA60821	(55)	NMCSADADAQLDAVLSAATETYSGLTPEQKAYVPAMFTAALNIQTSVNTVVRDF					
M1R-P33040	(55)	NMCSADADAQLDAVLSAATETYSGLTPEQKAYVPAMFTAALNIQTSVNTVVRDF					
Consensus	(55)	NMCSADADAQLDAVLSAATETYSGLTPEQKAYVPAMFTAALNIQTSVNTVVRDF					
							Section 3
	(109)	109	120	130	140	150	162
L1R-P07612	(109)	ENYVKQTCNSSAVVDNKLKIQNVIIIDECYGAPGSPTNLEFINTGSSKGNCAIKA					
L1R-AAA48076	(109)	ENYVKQTCNSSAVVDNKLKIQNVIIIDECYGAPGSPTNLEFINTGSSKGNCAIKA					
M1R-AAA60821	(109)	ENYVKQTCNSSAVVDNKLKIQNVIIIDECYGAPGSPTNLEFINTGSSKGNCAIKA					
M1R-P33040	(109)	ENYVKQTCNSSAVVDNKLKIQNVIIIDECYGAPGSPTNLEFINTGSSKGNCAIKA					
Consensus	(109)	ENYVKQTCNSSAVVDNKLKIQNVIIIDECYGAPGSPTNLEFINTGSSKGNCAIKA					
							Section 4
	(163)	163	170	180	190	200	216
L1R-P07612	(163)	LMQLTTKATTQIAPRQVAGTGVQFYMIVIGVIIAALFMYAKRMLFTSTNDKI					
L1R-AAA48076	(163)	LMQLTTKATTQIAPRQVAGTGVQFYMIVIGVIIAALFMYAKRMLFTSTNDKI					
M1R-AAA60821	(163)	LMQLTTKATTQIAPRQVAGTGVQFYMIVIGVIIAALFMYAKRMLFTSTNDKI					
M1R-P33040	(163)	LMQLTTKATTQIAPRQVAGTGVQFYMIVIGVIIAALFMYAKRMLFTSTNDKI					
Consensus	(163)	LMQLTTKATTQIAPRQVAGTGVQFYMIVIGVIIAALFMYAKRMLFTSTNDKI					
							Section 5
	(217)	217	230	240	250		
L1R-P07612	(217)	KLILANKENVHWTTYMDTFFRTSPMVIATTD MQN					
L1R-AAA48076	(217)	KLILANKENVHWTTYMDTFFRTSPMVIATTD MQN					
M1R-AAA60821	(217)	KLILANKENVHWTTYMDTFFRTSPMVIATTD IQN					
M1R-P33040	(217)	KLILANKENVHWTTYMDTFFRTSPMVIATTD IQN					
Consensus	(217)	KLILANKENVHWTTYMDTFFRTSPMVIATTD MQN					

FIGURE 3.

								Section 1
	(1)	1	10	20	30	40	54	
A27L-P11258	(1)	MDGTLFPGDDDLAIPATEFFSTKAAKKPDRKREQIVKADEDDNEETLKQRLTNL						
A27L-P20535	(1)	MDGTLFPGDDDLAIPATEFFSTKADKKPEAKREAIVKADEDDNEETLKQRLTNL						
A30L-P33816	(1)	MDGTLFPGDDDLAIPATEFFSTKAAKKPEAKREAIVKADGDDNEETLKQRLTNL						
A30L-AAA60882	(1)	MDGTLFPGDDDLAIPATEFFSTKAAKKPEAKREAIVKADGDDNEETLKQRLTNL						
Consensus	(1)	MDGTLFPGDDDLAIPATEFFSTKAAKKPEAKREAIVKADGDDNEETLKQRLTNL						
								Section 2
	(55)	55	60	70	80	90	108	
A27L-P11258	(55)	EKKITNVTTKFEQIEKCCCKRNDEVLFRLNHAETLRAAMISLAKKIDVQTGRRP						
A27L-P20535	(55)	EKKITNVTTKFEQIEKCCCKRNDEVLFRLNHAETLRAAMISLAKKIDVQTGRRP						
A30L-P33816	(55)	EKKITNVTTKFEQIEKCCCKRNDDVLFRLNHAETLRAAMISLAKKIDVQTGRRP						
A30L-AAA60882	(55)	EKKITNVTTKFEQIEKCCCKRNDDVLFRLNHAETLRAAMISLAKKIDVQTGRRP						
Consensus	(55)	EKKITNVTTKFEQIEKCCCKRNDDVLFRLNHAETLRAAMISLAKKIDVQTGRRP						
								Section 3
	(109)	<u>109</u>						
A27L-P11258	(109)	YE						
A27L-P20535	(109)	YE						
A30L-P33816	(109)	YE						
A30L-AAA60882	(109)	YE						
Consensus	(109)	YE						

FIGURE 4

A33R-A36Ralign

Section 1							
	(1)	1	10	20	30	40	54
A33R-H42520	(1)	MMTPENDEEQTSVFSATVYGDKIQGKNKRKRKRVIGLCIRISMVISL L SMITMSAF					
A33R-AAA48160	(1)	MMTPENDEEQTSVFSATVYGDKIQGKNKRKRKRVIGLCIRISMVISL L SMITMSAF					
A36R-P33850	(1)	MMTPENDEEQTSVFSATVYGDKIQGKNKRKRKRVIGICIRISMVISL L SMITMSAF					
A36R-AAA60888	(1)	MMTPENDEEQTSVFSATVYGDKIQGKNKRKRKRVIGICIRISMVISL L SMITMSAF					
Consensus	(1)	MMTPENDEEQTSVFSATVYGDKIQGKNKRKRKRVIGICIRISMVISL L SMITMSAF					
Section 2							
	(55)	55	60	70	80	90	108
A33R-H42520	(55)	LIVRLNQCMSANEAAITDAAVAVAAASSTHRKVASSTTQYDHKESCNGLYYQGS					
A33R-AAA48160	(55)	LIVRLNQCMSANEAAITDAAVAVAAASSTHRKVASSTTQYDHKESCNGLYYQGS					
A36R-P33850	(55)	LIVRLNQCMSANEAAITD - ATAVAAALSTHRKVASSTTQYKHQESCNGLYYQGS					
A36R-AAA60888	(55)	LIVRLNQCMSANEAAITD - ATAVAAALSTHRKVASSTTQYKHQESCNGLYYQGS					
Consensus	(55)	LIVRLNQCMSANEAAITDAAVAVAAASSTHRKVASSTTQYKHQESCNGLYYQGS					
Section 3							
	(109)	109	120	130	140	150	162
A33R-H42520	(109)	CYILHSDYQLFSDAKANCTAESSTLPNKSDVLITWLIDYVEDTWGSDGNPITKT					
A33R-AAA48160	(109)	CYILHSDYQLFSDAKANCTAESSTLPNKSDVLITWLIDYVEDTWGSDGNPITKT					
A36R-P33850	(108)	CYIFHSDYQLFSDAKANCTESSTLPNKSDVLTTWLIDYVEDTWGSDGNPITKT					
A36R-AAA60888	(108)	CYIFHSDYQLFSDAKANCTESSTLPNKSDVLTTWLIDYVEDTWGSDGNPITKT					
Consensus	(109)	CYILHSDYQLFSDAKANCTTESSTLPNKSDVLTTWLIDYVEDTWGSDGNPITKT					
Section 4							
	(163)	163	170	185			
A33R-H42520	(163)	TSDYQSDSDVSQEVRYFCVKTMN					
A33R-AAA48160	(163)	TSDYQSDSDVSQEVRYFCVKTMN					
A36R-P33850	(162)	TTDYQSDSDVSQEVRYFCVKTMN					
A36R-AAA60888	(162)	TTDYQSDSDVSQEVRYFCVKTMN					
Consensus	(163)	TSDYQSDSDVSQEVRYFCVKTMN					

FIGURE 5

Section 1							
	(1)	1	10	20	30	40	55
D8L-P04195	(1)	MPQQLSPINIETKKAISNARLKPLDIHYNESKPTTIQNTGKLVRINFKGGYISGG					
D8L-AAA48107	(1)	MPQQLSPINIETKKAISNARLKPLDIHYNESKPTTIQNTGKLVRINFKGGYISGG					
F8L-P33065	(1)	MSQQLSPINIETKKAISNARLKPLNIHYNESKPTTIQNTGKLVRINFKGGYLSGG					
F8L-AAA60846	(1)	MSQQLSPINIETKKAISNARLKPLNIHYNESKPTTIQNTGKLVRINFKGGYLSGG					
Consensus	(1)	MSQQLSPINIETKKAISNARLKPLNIHYNESKPTTIQNTGKLVRINFKGGYISGG					
Section 2							
	(56)	56	70	80	90	100	110
D8L-P04195	(56)	FLPNEYVLSSLHIYWGKEDDYGSNHLIDVYKYSGEINLVHWNKKKYSSYEEAKKH					
D8L-AAA48107	(56)	FLPNEYVLSSLHIYWGKEDDYGSNHLIDVYKYSGEINLVHWNKKKYSSYEEAKKH					
F8L-P33065	(56)	FLPNEYVLSSLHIYWGKEDDYGSNHLIDVYKYSGEINLVHWNKKKYSSYEEAKKH					
F8L-AAA60846	(56)	FLPNEYVLSSLHIYWGKEDDYGSNHLIDVYKYSGEINLVHWNKKKYSSYEEAKKH					
Consensus	(56)	FLPNEYVLSSLHIYWGKEDDYGSNHLIDVYKYSGEINLVHWNKKKYSSYEEAKKH					
Section 3							
	(111)	111	120	130	140	150	165
D8L-P04195	(111)	DDGLIIISIFLQVLDHKNVYFQKIVNQLDSIRSANTSAPFDSVFYLDNLLPSKLD					
D8L-AAA48107	(111)	DDGLIIISIFLQVSDHKNVYFQKIVNQLDSIRSANTSAPFDSVFYLDNLLPSTLD					
F8L-P33065	(111)	DDGLIIISIFLQVSDHKNVYFQKIVNQLDSIRTANTSAPFDSVFYLDNLLPSKLD					
F8L-AAA60846	(111)	DDGLIIISIFLQVSDHKNVYFQKIVNQLDSIRTANTSAPFDSVFYLDNLLPSKLD					
Consensus	(111)	DDGLIIISIFLQVSDHKNVYFQKIVNQLDSIRSANTSAPFDSVFYLDNLLPSKLD					
Section 4							
	(166)	166	180	190	200	210	220
D8L-P04195	(166)	YFTYLGTTINHSADAVWIIFPTPINIHSDQLSKFRTLSSSNHDGKPHYITENYR					
D8L-AAA48107	(166)	YFTYLGTTIKHSADAVWIIFPTPINIHSDQLSKFRTLSSSNHDGKPHYITENYR					
F8L-P33065	(166)	YFKYLGTTINHSADAVWIIFPTPINIHSDQLSKFRTLSSSNHEGKPHYITENYR					
F8L-AAA60846	(166)	YFKYLGTTINHSADAVWIIFPTPINIHSDQLSKFRTLSSSNHEGKPHYITENYR					
Consensus	(166)	YFTYLGTTINHSADAVWIIFPTPINIHSDQLSKFRTLSSSNHDGKPHYITENYR					
Section 5							
	(221)	221	230	240	250	260	275
D8L-P04195	(221)	NPYKLNDDTQVYYSGEIIIRAATTSPARENYFMRWLSDLRETCFSYYQKYIEENKT					
D8L-AAA48107	(221)	NPYKLNDDTQVYYSGEIIIRAATTSPARENYFMRWLSDLRETCFSYYQKYIEGNKT					
F8L-P33065	(221)	NPYKLNDDTEVYYSGEIIIRAATTSPARENYFMRWLSDLRETCFSYYQKYIEGNKT					
F8L-AAA60846	(221)	NPYKLNDDTEVYYSGEIIIRAATTSPARENYFMRWLSDLRETCFSYYQKYIEGNKT					
Consensus	(221)	NPYKLNDDTQVYYSGEIIIRAATTSPARENYFMRWLSDLRETCFSYYQKYIEGNKT					
Section 6							
	(276)	276	290	304			
D8L-P04195	(276)	FAIIAIVFVFILTAILFFMSRRYSREKQN					
D8L-AAA48107	(276)	FAIIAIVFVFILTAILFLMSRRYSREKQN					
F8L-P33065	(276)	FAIIAIVFVYIILTAILFLMSRRYSREKQN					
F8L-AAA60846	(276)	FAIIAIVFVYIILTAILFLMSRRYSREKQN					
Consensus	(276)	FAIIAIVFVFILTAILFLMSRRYSREKQN					

FIGURE 6

Section 1									
	(1)	1	10	20	30	40	54		
B5R-JQ1799	(1)	MKTISVVTLL	CVLP	PAVVYSTCTVPTM	NAKLTSTETSFNDKQKV	TFTCDQGYHS			
B5R-D42526	(1)	MKTISVVTLL	CVLP	PAVVYSTCTVPTM	NAKLTSTETSFNNNQKV	TFTCDQGYHS			
B7R-NP_042219	(1)	MKTISVVTLL	CVLP	PAVVYSTCTVPTM	NAKLTSTETSFNDKQKV	TFTCDSGYYS			
B7R-CAA49116	(1)	MKTISVVTLL	CVLP	PAVVYSTCTVPTM	NAKLTSTETSFNDKQKV	TFTCDSGYYS			
B7R-G36855	(1)	MKTISVVTLL	CVLP	PAVVYSTCTVPTM	NAKLTSTETSFNDKQKV	TFTCDSGYYS			
B7R-2015436GX	(1)	MKTISVVTLL	CVLP	PAVVYSTCTVPTM	NAKLTSTETSFNDKQKV	TFTCDSGYYS			
Consensus	(1)	MKTISVVTLL	CVLP	PAVVYSTCTVPTM	NAKLTSTETSFNDKQKV	TFTCDSGYYS			
Section 2									
	(55)	55	60	70	80	90	108		
B5R-JQ1799	(55)	SDPNAVCETD	CKWKYENPCKKMCTVSDY	ISELYNKPLYEVNSTMTL	SCNGETKYF				
B5R-D42526	(55)	SDPNAVCETD	CKWKYENPCKKMCTVSDY	ISELYNKPLYEVNSTMTL	SCNGETKYF				
B7R-NP_042219	(55)	LDPNAVCETD	CKWKYENPCKKMCTVSDY	VSELYNKPLYEVNAIITL	ICKDETKYF				
B7R-CAA49116	(55)	LDPNAVCETD	CKWKYENPCKKMCTVSDY	VSELYNKPLYEVNAIITL	ICKDETKYF				
B7R-G36855	(55)	LDPNAVCETD	CKWKYENPCKKMCTVSDY	VSELYNKPLYEVNAIITL	ICKDETKYF				
B7R-2015436GX	(55)	LDPNAVCETD	CKWKYENPCKKMCTVSDY	VSELYNKPLYEVNAIITL	ICKDETKYF				
Consensus	(55)	LDPNAVCETD	CKWKYENPCKKMCTVSDY	VSELYNKPLYEVNAIITL	ICKDETKYF				
Section 3									
	(109)	109	120	130	140	150	162		
B5R-JQ1799	(109)	RCEEKNGNTS	WN	DTVTC	PNAECQPLQLEHGSCQ	PVKEKYSFGEYMTIN	CDVGYE		
B5R-D42526	(109)	RCEEKNGNTS	WN	DTVTC	PNAECQPLQLEHGSCQ	PVKEKYSFGEYMTIN	CDVGYE		
B7R-NP_042219	(109)	RCEEKNGNTS	WN	DTVTC	PNAECQSLQLDHGSCQ	PVKEKYSFGEHITIN	CDVGYE		
B7R-CAA49116	(109)	RCEEKNGNTS	WN	DTVTC	PNAECQSLQLDHGSCQ	PVKEKYSFGEHITIN	CDVGYE		
B7R-G36855	(109)	RCEEKNGNTS	WN	DTVTC	PNAECQSLQLDHGSCQ	PVKEKYSFGEHITIN	CDVGYE		
B7R-2015436GX	(109)	RCEEKNGNTS	WN	DTVTC	PNAECQSLQLDHGSCQ	PVKEKYSFGEHITIN	CDVGYE		
Consensus	(109)	RCEEKNGNTS	WN	DTVTC	PNAECQSLQLDHGSCQ	PVKEKYSFGEHITIN	CDVGYE		
Section 4									
	(163)	163	170	180	190	200	216		
B5R-JQ1799	(163)	VIGASYISCT	ANSWN	VIPSCQQKCDMP	SLNGLISGSTFSIGGVI	HL	SCKSGFT		
B5R-D42526	(163)	VIGASYISCT	ANSWN	VIPSCQQKCDIP	SLNGLISGSTFSIGGVI	HL	SCKSGFI		
B7R-NP_042219	(163)	VIGASYITCT	ANSWN	VIPSCQQKCDIP	SLNGLISGSTFSIGGVI	HL	SCKSGFI		
B7R-CAA49116	(163)	VIGASYITCT	ANSWN	VIPSCQQKCDIP	SLNGLISGSTFSIGGVI	HL	SCKSGFI		
B7R-G36855	(163)	VIGASYITCT	ANSWN	VIPSCQQKCDIP	SLNGLISGSTFSIGGVI	HL	SCKSGFI		
B7R-2015436GX	(163)	VIGASYITCT	ANSWN	VIPSCQQKCDIP	SLNGLISGSTFSIGGVI	HL	SCKSGFI		
Consensus	(163)	VIGASYITCT	ANSWN	VIPSCQQKCDIP	SLNGLISGSTFSIGGVI	HL	SCKSGFI		
Section 5									
	(217)	217	230	240	250	260	270		
B5R-JQ1799	(217)	LTGSPSSTC	IDGKWN	PVLPIC	VRTNEEFDPVDDGPDD	ETDLSKLSKD	VVQYEQE		
B5R-D42526	(217)	LTGSPSSTC	IDGKWN	PVLPIC	VRTNEEFDPVDDGPDD	ETDLSKLSKD	VVQYEQE		
B7R-NP_042219	(217)	LTGSPSSTC	IDGKWN	PVLPIC	IRSNEEFDPVEDGPDD	ETDLSKLSKD	VVQYEQE		
B7R-CAA49116	(217)	LTGSPSSTC	IDGKWN	PVLPIC	IRSNEEFDPVEDGPDD	ETDLSKLSKD	VVQYEQE		
B7R-G36855	(217)	LTGSPSSTC	IDGKWN	PVLPIC	IRSNEEFDPVEDGPDD	ETDLSKLSKD	VVQYEQE		
B7R-2015436GX	(217)	LTGSPSSTC	IDGKWN	PVLPIC	IRSNEEFDPVEDGPDD	ETDLSKLSKD	VVQYEQE		
Consensus	(217)	LTGSPSSTC	IDGKWN	PVLPIC	IRSNEEFDPVEDGPDD	ETDLSKLSKD	VVQYEQE		

FIGURE 7

---

	(271)	271	280	290	300	317
B5R-JQ1799	(271)	IESLEATYHII	IIVALTIMGVIFLISVIVLVCSCDKNNDQYKFHKLLP			
B5R-D42526	(271)	IESLEATYHII	IIVALTIMGVIFLISVIVLVCSCDKNNDQYKFHKLLP			
B7R-NP_042219	(271)	IESLEATYHII	IIVALTIMGVIFLISVIVLVCSCNKNNDQYKFHKLLL			
B7R-CAA49116	(271)	IESLEATYHII	IIVALTIMGVIFLISVIVLVCSCNKNNDQYKFHKLLL			
B7R-G36855	(271)	IESLEATYHII	IIVALTIMGVIFLISVIVLVCSCNKNNDQYKFHKLLL			
B7R-2015436GX	(271)	IESLEATYHII	IIVALTIMGVIFLISVIVLVCSCNKNNDQYKFHKLLL			
Consensus	(271)	IESLEATYHII	IIVALTIMGVIFLISVIVLVCSCNKNNDQYKFHKLLL			

FIGURE 7 CONTINUED

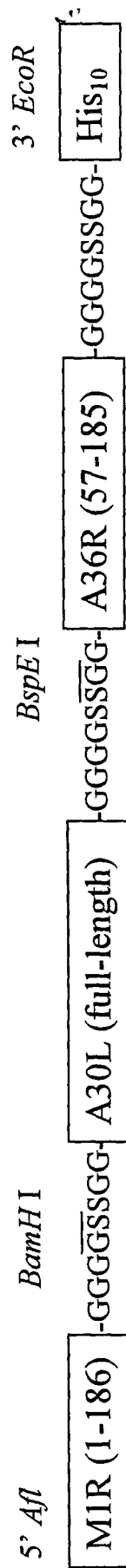


## H5R-I5Ralign

Section 1							
	(1)	1	10	20	30	40	55
H5R-P07242	(1)	MAWSITNKADTSSFTKMAEIRAHLKNSAENKDKNEDIFPEDVIIPSTKPKTKRAT					
H5R-E42514	(1)	MAWSITNKADTSSFTKMAEIRAHLKNSAENKDKNEDIFPEDVIIPSTKPKTKRAT					
I5R-P33062	(1)	MAWSITNKADTSSFTKMAEIRAHLRNSAENKDKNDDIFPEDVIIPSTKPKTKRAT					
I5R-AAA60836	(1)	MAWSITNKADTSSFTKMAEIRAHLRNSAENKDKNDDIFPEDVIIPSTKPKTKRAT					
Consensus	(1)	MAWSITNKADTSSFTKMAEIRAHLKNSAENKDKNDDIFPEDVIIPSTKPKTKRAT					
Section 2							
	(56)	56	70	80	90	100	110
H5R-P07242	(56)	TPRKPAATKRSTKKEE-----VEEEVVEEYHQTTEKNSP----SPGVSDIVESV					
H5R-E42514	(56)	TPRKPAATKRSTKKEE-----VEEEVVEEYHQTTEKNSP----SPGVGDIVESV					
I5R-P33062	(56)	TPRKPAATKRSTKKDKKEEVEEEVVEEYHQTTEENSPPPSSSPGVGNIVESV					
I5R-AAA60836	(56)	TPRKPAATKRSTKKDKKEEV-EEEVVEEYHQTTEENSPPPSSSPGVGDIVESV					
Consensus	(56)	TPRKPAATKRSTKKDKKEEVEEEVVEEYHQTTEKNSPPPSSSPGVGDIVESV					
Section 3							
	(111)	111	120	130	140	150	165
H5R-P07242	(102)	AAVELDDSDGDD-----EPMVQVEAGKVNHSARSDLSDLKVATDNIVKDLK					
H5R-E42514	(102)	AAVELDDSDGDD-----EPMVQVEAGKVNHSARSDLSDLKVATDNIVKDLK					
I5R-P33062	(111)	TAVELDDSNDDDDNDNDNDNEPMVQVEAGKVNHSARSDLSDLKVATDNIVKDLK					
I5R-AAA60836	(110)	TAVELDDSNDDDDNDNDNDNEPMVQVEAGKVNHSARSDLSDLKVATDNIVKDLK					
Consensus	(111)	TAVELDDSNDDDDNDNDNDNEPMVQVEAGKVNHSARSDLSDLKVATDNIVKDLK					
Section 4							
	(166)	166	180	190	200	210	220
H5R-P07242	(148)	KIITRISAVSTVLEDVQAAGISRQFTSMTKAITTSLDLVTEGKSKVVRKKVKTCK					
H5R-E42514	(148)	KIITRISAVSTVLEDVQAAGISRQFTSMTKAITTSLDLVTEGKSKVVRKKVKTCK					
I5R-P33062	(166)	KIITRISAVSTVLEDVQAAGISRQFTSMTKSITTLSDLVTEGKSKVVRKKVKTCK					
I5R-AAA60836	(165)	KIITRISAVSTVLEDVQAAGISRQFTSMTKSITTLSDLVTEGKSKVVRKKVKTCK					
Consensus	(166)	KIITRISAVSTVLEDVQAAGISRQFTSMTKAITTSLDLVTEGKSKVVRKKVKTCK					
Section 5							
	(221)	<u>221</u>					
H5R-P07242	(203)	K					
H5R-E42514	(203)	K					
I5R-P33062	(221)	K					
I5R-AAA60836	(220)	K					
Consensus	(221)	K					

FIGURE 8

Figure 9



**Schematic representation of LAA polypeptide construct.** Respective coding regions for variola virus surface proteins M1R, A30L and A36R were first amplified with PCR using vaccinia virus genome as template. PCR-based mutagenesis was carried out to convert amino acid residues to those found in variola homologs. The coding sequence for LAA was assembled by in-frame ligation of three components, M1R<sub>1-186</sub>, A30L full-length and A36R<sub>57-185</sub>, facilitated by the designed BamHI and BspEI restriction sites in the spacer-linker sequence. The 5' end of the construct has an Afl II restriction site and consensus Kozak sequence while a 10 histidine tag and EcoRI site were engineered at the 3' end of the construct.